#58

SEQUENCE LISTING

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LERNER, Richard A.

<120> A NEW METHOD FOR TAPPING THE
IMMUNOLOGICAL REPERTOIRE

<130> 062710024DVUS01

B1

<140> 09/726,650
<141> 2000-11-28

<150> 07/933,958
<151> 1992-08-21

<150> 07/799,770
<151> 1991-11-27

<150> 07/533,103
<151> 1990-06-04

<160> 106

<170> FastSEQ for Windows Version 4.0

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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
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```
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
```

```
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Asp Tyr Pro His Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
```

```
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Phe
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Arg Tyr Asp Gly Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<400> 6

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Phe Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Arg Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Leu Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Val Tyr Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
```

```
                85                  90                  95
Tyr Cys Ala Arg Asp Ala Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Phe Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Val Tyr Gly Tyr Asp Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120

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<223> HPCG11-hybridoma

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Ile Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ser Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
```

```
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<223> HPCG132-hybridoma

<400> 10

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Ile Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<400> 11

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
```

```
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<222> (1)...(123)
<223> S63-myeloma protein

<400> 12

```
Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<400> 13

```
Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
```

```
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

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<400> 14

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 15
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<223> H8-myeloma protein

<400> 15

```
Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
```

```
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Tyr Tyr Gly Asn Ser Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<223> M603-myeloma protein

<400> 16

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Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Gly Asn Lys Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Trp Tyr Phe Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<400> 17

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```
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Pro Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Phe Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asn Tyr Tyr Lys Tyr Asp Leu Trp Tyr Val Asp Val
            100                 105                 110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<223> M511-myeloma protein

<400> 18

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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Tyr Met Glu Trp Val Arg Gln Pro Ser Gly Lys Arg Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ser Arg Asn Lys Ala Asn Asp Tyr Thr Thr Glu Tyr Ser Ala
    50                  55                  60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Ile
65                  70                  75                  80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Ala Arg Asp Gly Asp Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp
            100                 105                 110
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 19
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<220>
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<223> M167-myeloma protein

<400> 19
Glu Val Val Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asp Phe
            20   25   30
Tyr Met Glu Trp Val Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Ile
        35   40   45
Ala Ala Ser Arg Ser Lys Ala His Asp Tyr Thr Arg Glu Tyr Ser Ala
    50   55   60
Ser Val Lys Gly Arg Phe Ile Val Ser Arg Asp Thr Ser Gln Ser Val
65   70   75   80
Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Thr Tyr
                85   90   95
Tyr Cys Thr Arg Asp Ala Asp Tyr Gly Asn Ser Tyr Phe Gly Tyr Phe
            100   105   110
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115   120   125

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actggctact ccatcaccag tgcttattac tggaactgga tccggcagtt   110

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tctggccaca ccttgactag ttactggata cactgggtaa aanagaggcc   110

<210> 22
<211> 109
<212> DNA
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<220>
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<222> (1)...(109)
<223> n=A,T,C or G

<400> 22
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tctggataca ttcacnagct atgttataca ctgggtgaag cagaagcct   109

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<211> 110
<212> DNA
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<400> 23
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tctggataca cattcaccag ctatgttatg cgctgggtga agcacaagcc 110

<210> 24
<211> 110
<212> DNA
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<220>
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tctggctaca ccttcacnag ctactatatg tactgggtga agcagaggcc 110

<210> 25
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tctggctact ccttcacnag ctactggatg aactgggtga agcagaggcc 110

<210> 26
<211> 110
<212> DNA
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<220>
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<223> n=A,T,C or G

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tctcgtactc cttcaccagc tcctgataac tgggtgaagc agaggcctgg 110

<210> 27
<211> 110

<212> DNA
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<220>
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<223> n=A,T,C or G

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tcaggattcg atttnagnag atactggatg aattgggtcc ggcagctcca 110

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<211> 110
<212> DNA
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<220>
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<222> (1)...(110)
<223> n=A,T,C or G

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tcaggattcg atttnagnag ataatggatg agttgggttc ggcaggctcc 110

<210> 29
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<220>
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<223> n= A,T,C'or G

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tcaggattcg atttnagnag atactggatg agttgggtcc ggcagctcca 110

<210> 30
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<212> DNA
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<220>
<221> misc_feature
<222> (1)...(110)
<223> n=A,T,C or G

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tcaggattcg atttnagnag atactggatg agttgggtcc ggcagctcca 110

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<222> (1)...(110)
<223> n=A,T,C or G

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<223> n=A,T,C or G

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<210> 34
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<222> (1)...(110)
<223> n=A,T,C or G

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tcaggctatt ccttcaccag ctactggatg cactgggtga aacagaggcc 110

<210> 35
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<400> 35
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tctggctaca cctcttcttc cttctggctg cactggataa aagaaggcct 110

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<223> n=A,T,C or G

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ctggttactc attttctntc tactttgtga actgggtgat gcagagccat 110

<210> 37
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<212> DNA
<213> Mouse

<400> 37
ctcgagtcag gggctgaact ggtgaagcct ggggttcagt aagttgtcct gaaggcttct 60
ggctacacct tcaccggcta ctatatgtac tgggtgaagc agaggcctgg 110

<210> 38
<211> 91
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 38
ggccgcaaat tctatttcaa ggagacagtc ataatgaaat acctattgcc tacggcagcc 60
gctggattgt tattactcgc tgcccaacca g 91

<210> 39
<211> 87
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 39
cgtttaagat aaagttcctc tgtcagtatt actttatgga taacggatgc cgtcggcgac 60
ctaacaataa tgagcgacgg gttggtc 87

<210> 40
<211> 82
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 40
ccatggccca ggtgaaactg ctcgagattt ctagactagt tacccgtacg acgttccgga 60
ctacggttct taatagaatt cg 82

<210> 41
<211> 86
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 41
ggtaccgggt ccactttgac gagctctaaa gatctgatca atgggcatgc tgcaaggcct 60
gatgccaaga attatcttaa gcaggt 86

<210> 42
<211> 91
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 42
ggccgcaaat tctatttcaa ggagacagtc ataatgaaat acctattgcc tacggcagcc 60
gctggattgt tattactcgc tgcccaacca g 91

<210> 43
<211> 87
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 43
cgtttaagat aaagttcctc tgtcagtatt actttatgga taacggatgc cgtcggcgac 60
ctaacaataa tgagcgacgg gttggtc 87

<210> 44
<211> 46

<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 44
ccatggccca ggtgaaactg ctcgagaatt ctagactagt taatag 46

<210> 45
<211> 50
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 45
ggtaccgggt ccactttgac gagctcttaa gatctgatca attatcagct 50

<210> 46
<211> 131
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 46
tgaattctaa actagtcgcc aaggagacag tcataatgaa atacctattg cctacggcag 60
ccgctggatt gttattactc gctgcccaac cagccatggc cgagctcgtc agttctagag 120
ttaagcggcc g 131

<210> 47
<211> 131
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 47
tgaattctaa actagtcgcc aaggagacag tcataatgaa atacctattg cctacggcag 60
ccgctggatt gttattactc gctgcccaac cagccatggc cgagctcgtc agttctagag 120
ttaagcggcc g 131

<210> 48
<211> 140
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 48
tcgaacttaa gatttgatca gcggttcctc tgtcagtatt actttatgga taacggatgc 60
cgtcggcgac ctaacaataa tgagcgacgg gttggtcggt taccggctcg agcagtcaag 120
atctcaattc gccggcagct 140

<210> 49
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 49
aggtccagct gctcgagtct gg 22

<210> 50
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 50
aggtgaaact tctcgagtca gg 22

<210> 51
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 51
aggtccagct gctcgagtct gg 22

<210> 52
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 52
aggtccagct gctcgagtca gg 22

<210> 53
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 53
aggtccagct tctcgagtct gg 22

<210> 54
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 54
aggtccagct tctcgagtca gg 22

<210> 55
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 55
aggtccaact gctcgagtct gg 22

<210> 56
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 56
aggtccaact gctcgagtca gg 22

<210> 57
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 57
aggtccaact tctcgagtct gg 22

<210> 58
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 58
aggtccaact tctcgagtca gg 22

<210> 59
<211> 20
<212> DNA
<213> Unknown

<220>
<223> Synthetic
5' degenerate primer containing inosine at 4
degenerate positions

<221> misc_feature
<222> (1)...(20)
<223> n=A,T,C or G

<400> 59
aggtnnanct nctcgagtct 20

<210> 60
<211> 20
<212> DNA
<213> Unknown

<220>
<223> Synthetic
5' degenerate primer containing inosine at 4
degenerate positions

<221> misc_feature
<222> (1)...(20)
<223> n=A,T,C or G

<400> 60
aggtnnanct nctcgagtca 20

<210> 61
<211> 19
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 61
gcccaaggat gtgctcacc 19

<210> 62
<211> 39

<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 62
ctattagaat tcaacggtaa cagtggtgcc ttggcccca 39

<210> 63
<211> 39
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 63
ctattaacta gtaacggtaa cagtggtgcc ttggcccca 39

<210> 64
<211> 19
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 64
ctcagtatgg tggttgtgc 19

<210> 65
<211> 26
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 65
gctactagtt ttgatttcca ccttgg 26

<210> 66
<211> 23
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 66
cagccatggc cgacatccag atg 23

<210> 67

<211> 30
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 67
aattttacta gtcaccttgg tgctgctggc 30

<210> 68
<211> 39
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 68
tatgcaacta gtacaaccac aatccctggg cacaatttt 39

<210> 69
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 69
ccagttccga gctcgttgtg actcaggaat ct 32

<210> 70
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 70
ccagttccga gctcgtgttg acgcagccgc cc 32

<210> 71
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 71
ccagttccga gctcgtgctc acccagtctc ca 32

<210> 72
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 72
ccagttccgc gctccagatg acccagtctc ca 32

<210> 73
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 73
ccagatgtga gctcgtgatg acccagactc ca 32

<210> 74
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 74
ccagatgtga gctcgtcatg acccagtctc ca 32

<210> 75
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 75
ccagatgtga gctcttgatg acccaaactc aa 32

<210> 76
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 76
ccagatgtga gctcgtgata acccaggatg aa 32

<210> 77
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 77
gcagcattct agagtttcag ctccagcttg cc 32

<210> 78
<211> 33
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 78
ccgccgtcta gaacactcat tcctgttgaa gct 33

<210> 79
<211> 33
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 79
ccgccgtcta gaacattctg caggagacag act 33

<210> 80
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 80
ccagttccga gctcgtgatg acacagtctc ca 32

<210> 81
<211> 34
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 81

gcgccgtcta gaattaacac tcattcctgt tgaa 34

<210> 82
<211> 38
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 82
ctattaacta gtaacggtaa cagtggtgcc ttgcccca 38

<210> 83
<211> 30
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 83
aggcttacta gtacaatccc tgggcacaat 30

<210> 84
<211> 29
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 84
gccgctctag aacactcatt cctgttgaa 29

<210> 85
<211> 22
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<221> misc_feature
<222> (1)...(22)
<223> N=Degenerate 5' primer containing inosinine at 4
degenerate positions.

<400> 85
aggtnnanct nctcgagtct gc 22

<210> 86
<211> 22
<212> DNA

<213> Unknown

<220>
<223> Synthetic

<221> misc_feature
<222> (1)...(22)
<223> n= Degenerate 5' primer containing inosine at 4'
degenerate positions.

<400> 86
aggtnnanct nctcgagtca gc 22

<210> 87
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 87
ggccgcaaat tctatttcaa ggagacagtc at 32

<210> 88
<211> 36
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 88
aatgaaatac ctattgccta cggcagccgc tggatt 36

<210> 89
<211> 28
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 89
gttattactc gctgcccaac catggccc 28

<210> 90
<211> 38
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 90
aggtgaaact gctcgagaat tctagactag gttaatag 38

<210> 91
<211> 30
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 91
tcgactatta actagtctag aattctcgag 30

<210> 92
<211> 29
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 92
cagtttcacc tgggccatgg ctggttggg 29

<210> 93
<211> 40
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 93
cagcgagtaa taacaatcca gcggctgccg taggcaatag 40

<210> 94
<211> 38
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 94
gtatttcatt atgactgtct ccttgaaata gaatttgc 38

<210> 95
<211> 40
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 95
aggtgaaact gctcgagatt tctagactag ttacccgtac 40

<210> 96
<211> 33
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 96
gacgttccgg actacggttc ttaatagaat tcg 33

<210> 97
<211> 28
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 97
tcgacgaatt ctattaagaa ccgtagtc 28

<210> 98
<211> 38
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 98
cggaacgtcg tacgggtaac tagtctagaa atctcgag 38

<210> 99
<211> 34
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 99
tgaattctaa actagtcgcc aaggagacag tcat 34

<210> 100
<211> 37
<212> DNA
<213> Unknown

<220>

<223> Synthetic

<400> 100
aatgaaataa cctattgcct acggcagccg ctggatt 37

<210> 101
<211> 31
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 101
gttattactc gctgcccaac cagccatggc c 31

<210> 102
<211> 30
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 102
gagctcgtca gttctagagt taagcggccg 30

<210> 103
<211> 48
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 103
gtatttcatt atgactgtct ccttggcgac tagtttagaa ttcaagct 48

<210> 104
<211> 40
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 104
cagcgagtaa taacaatcca gcggctgccg taggcaatag 40

<210> 105
<211> 27
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 105
tgacgagctc ggccatggct ggttggg 27

<210> 106
<211> 24
<212> DNA
<213> Unknown

<220>
<223> Synthetic

<400> 106
tcgacggccg cttaactcta gaac 24